



SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Screening Method Using CD100

<130> 46342/56,721

<140> 10/009,330

<141> 2001-12-03

<150> JP 11-157111

<151> 1999-06-03

<160> 10

<210> 1

<211> 861

<212> PRT

<213> Mouse

<400> 1

Met Arg Met Cys Ala Pro Val Arg Gly Leu Phe Leu Ala Leu Val Val
1 5 10 15
Val Leu Arg Thr Ala Val Ala Phe Ala Pro Val Pro Arg Leu Thr Trp
20 25 30
Glu His Gly Glu Val Gly Leu Val Gln Phe His Lys Pro Gly Ile Phe
35 40 45
Asn Tyr Ser Ala Leu Leu Met Ser Glu Asp Lys Asp Thr Leu Tyr Val
50 55 60
Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
65 70 75 80
Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ser Lys
85 90 95
Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
100 105 110
Arg Val Leu Gln Pro Leu Ser Ser Thr Ser Leu Tyr Val Cys Gly Thr
115 120 125
Asn Ala Phe Gln Pro Thr Cys Asp His Leu Asn Leu Thr Ser Phe Lys
130 135 140
Phe Leu Gly Lys Ser Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro
145 150 155 160
Ala His Ser Tyr Thr Ser Val Met Val Gly Gly Glu Leu Tyr Ser Gly
165 170 175
Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
180 185 190
Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu
195 200 205
Pro Ser Phe Val Phe Ala Asp Val Ile Gln Lys Ser Pro Asp Gly Pro
210 215 220
Glu Gly Glu Asp Asp Lys Val Tyr Phe Phe Phe Thr Glu Val Ser Val
225 230 235 240

Glu Tyr Glu Phe Val Phe Lys Leu Met Ile Pro Arg Val Ala Arg Val
 245 250 255
 Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr
 260 265 270
 Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Lys Pro Asp Ser Gly Leu
 275 280 285
 Val Phe Asn Ile Leu Gln Asp Val Phe Val Leu Arg Ala Pro Gly Leu
 290 295 300
 Lys Glu Pro Val Phe Tyr Ala Val Phe Thr Pro Gln Leu Asn Asn Val
 305 310 315 320
 Gly Leu Ser Ala Val Cys Ala Tyr Thr Leu Ala Thr Val Glu Ala Val
 325 330 335
 Phe Ser Arg Gly Lys Tyr Met Gln Ser Ala Thr Val Glu Gln Ser His
 340 345 350
 Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Thr Pro Arg Pro Gly
 355 360 365
 Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu
 370 375 380
 Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met
 385 390 395 400
 Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Lys Leu Ile Lys Lys
 405 410 415
 Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp
 420 425 430
 Gly Thr Phe Tyr Asp Val Met Phe Ile Ser Thr Asp Arg Gly Ala Leu
 435 440 445
 His Lys Ala Val Ile Leu Thr Lys Glu Val His Val Ile Glu Glu Thr
 450 455 460
 Gln Leu Phe Arg Asp Phe Glu Pro Val Leu Thr Leu Leu Leu Ser Ser
 465 470 475 480
 Lys Lys Gly Arg Lys Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val
 485 490 495
 Gln Ala Pro Leu Ala Phe Cys Glu Lys His Gly Ser Cys Glu Asp Cys
 500 505 510
 Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Ala Ile Lys Ala
 515 520 525
 Cys Val Thr Leu His Gln Glu Glu Ala Ser Ser Arg Gly Trp Ile Gln
 530 535 540
 Asp Met Ser Gly Asp Thr Ser Ser Cys Leu Asp Lys Ser Lys Glu Ser
 545 550 555 560
 Phe Asn Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys
 565 570 575
 Phe Gln Lys Ser Asn Leu Ala Arg Val Val Trp Lys Phe Gln Asn Gly
 580 585 590
 Glu Leu Lys Ala Ala Ser Pro Lys Tyr Gly Phe Val Gly Arg Lys His
 595 600 605
 Leu Leu Ile Phe Asn Leu Ser Asp Gly Asp Ser Gly Val Tyr Gln Cys
 610 615 620
 Leu Ser Glu Glu Arg Val Arg Asn Lys Thr Val Ser Gln Leu Leu Ala
 625 630 635 640
 Lys His Val Leu Glu Val Lys Met Val Pro Arg Thr Pro Pro Ser Pro
 645 650 655

Thr Ser Glu Asp Val Gln Thr Glu Gly Ser Lys Ile Thr Ser Lys Met
660 665 670
Pro Val Gly Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Leu Trp
675 680 685
Ala Thr Ser Pro Arg Ala Ala Thr Leu Pro Pro Lys Ser Ser Ser Gly
690 695 700
Thr Ser Cys Glu Pro Lys Met Val Ile Asn Thr Val Pro Gln Leu His
705 710 715 720
Ser Glu Lys Thr Val Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu Met
725 730 735
Ser Leu Leu Leu Phe Ile Phe Val Leu Phe Leu Cys Leu Phe Ser Tyr
740 745 750
Asn Cys Tyr Lys Gly Tyr Leu Pro Gly Gln Cys Leu Lys Phe Arg Ser
755 760 765
Ala Leu Leu Leu Gly Lys Lys Thr Pro Lys Ser Asp Phe Ser Asp Leu
770 775 780
Glu Gln Ser Val Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser Gln
785 790 795 800
Gln Asn Gly Asp His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu Thr
805 810 815
Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp Ser
820 825 830
Gln Arg Ile Asp Glu Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys
835 840 845
Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
850 855 860

<210> 2
<211> 2769
<212> DNA
<213> Mouse

<400> 2
gaattcggca cgaggccatc catgtgtgcc cgttgctgaa ggcctcggtg gcccctgc
cc 60
atgaggatgt gtgccccgt tagggggctg ttcttggccc tggtggtagt gttgagaa
cc 120
gccccatgttttgcacatgt gcctcggtc acctggaaac atggagaggt aggtctgg
tg 180
cagtttcaca agccaggcat ctttaactac tcggcattgc tgatgagtga ggacaaag
ac 240
actctgtatg taggcgccccg ggaagcagtc tttgcagtga atgcgctgaa catctctg
ag 300
aagcaacatg agtatattg gaaggtctct gaagacaaaa aatccaagtg tgcagaga
ag 360
ggaaatcaa agcagacgga atgcctaaac tacattcgag tactacagcc actaagca
gc 420
acttccctct atgtgtgtgg gaccaatgcg ttccagccca cctgtgacca cctgaact
tg 480
acatccttca agtttctggg gaaaagtgaa gatggcaaag gaagatgccc ctgcacc
cc 540
gccccacagct acacatcagt catggttggg ggcgagctct actctgggac gtcctata

at 600
ttcttggca gtgaacccat catctctcg aactttccc acagtccctt gaggacgg
ag 660
tatgccatcc cgtggctgaa cgagcctagc ttcgtctttg ctgacgtgat ccagaaaa
gc 720
ccagatggc cggagggtga agatgacaag gtctacttct ttttacgga ggtatccg
tg 780
gagtacgaat tcgtcttcaa gttgatgatc ccgcgagttg ccaggggtgtg caagggcg
ac 840
cagggcggcc tgccgacttt gcaaaaaaaag tggacctcct tcctaaaggc caggctga
tc 900
tgctccaagc cagacagtgg cctggcttc aacatacttc aggtgtgtt tgtgctga
gg 960
gccccggggcc tcaaggagcc tgtgttctat gcggtctca ccccacagct gaacaatg
tg 1020
ggtctgtcag cgggtgtgcgc ctacacactg gccacggtgg aggcagtctt ctcccgta
ga 1080
aagtacatgc agagtgccac agtggagcag tctcacacca agtgggtgcg ctacaatg
gc 1140
ccagtgcaca ctccccgacc tggagcgtgt atcgacagtg aggcccgggc agccaaact
ac 1200
accagctcct tgaatctccc agacaaaaca ctgcagttt taaaagacca cccttga
tg 1260
gatgactcag tgaccccgat agacaacaga cccaagctga tcaaaaaaga tgtaaact
ac 1320
acccagatag tggtagacag gaccaggcc ctggatggga ctttctacga cgtcatgt
tc 1380
atcagcacag accggggagc tctgcataaa gcagtcatcc tcacaaaaga ggtgcatt
tc 1440
atcgaggaga cccaaactctt ccggactct gaaccggtcc taactctgct gctatcgt
ca 1500
aagaagggga ggaagttgt ctatgcaggc tccaaactctg gagtggtcca agcgcccc
tg 1560
gcattctgcg aaaagcacgg tagctgtgaa gactgtgtgt tagcacggga cccctact
gt 1620
gcctggagcc cagccatcaa ggcctgtgtt accctgcacc aggaagaggc ctccagca
gg 1680
ggctggattc aggacatgag cggtgacaca tcctcatgcc tggataagag taaagaaa
gt 1740
ttcaaccaggc atttttcaa gcacggcgacagcgaaac tcaaattttt ccaaaagt
cc 1800
aacctagccc gggtggtatg gaagttccag aatggcgagt tgaaggccgc aagtccca
ag 1860
tacggcttg tggcaggaa gcacctgctc atcttcaacc tgcggacgg agacagcg
gc 1920
gtgtaccagt gcctgtcaga ggaaagggtg aggaataaaa cggtctccca gctgctgg
cc 1980
aagcacgttc tggaaagtgaa gatggtaccc cggacccccc cctcacctac ctcagagg
at 2040
gttcagacag aaggttagtaa gatcacatcc aaaatgcccgg ttggatctac ccaggggt
cc 2100
tctcccccta ccccggtctt gtggcaacc tccccagag ccgcacccct acctccca

ag 2160
tcctcctccg gcacatcctg tgaaccaaag atggcatca acacggtccc ccagctcc
ac 2220
tcagagaaga cggtgtatct caagtccagt gacaaccgcc tgctcatgtc tctcctcc
tc 2280
ttcatcttg tcctcttcct ctgcctctt tcctacaact gctacaaggg ctacctgc
cc 2340
ggacagtgtctaaaattccg ctcagccctg ctgcttggaa agaaaacacc caagtcag
ac 2400
ttctctgacc tggagcagag tgtgaaggag acactggtcg agcctggag cttctccc
ag 2460
cagaacggcg accaccccaa gccagccctg gatacgggct atgaaacgga gcaggaca
cc 2520
atcaccagca aagtccccac ggatcgtgag gactcgcaac ggatcgatga actctctg
cc 2580
cgggacaaac cggttcatgt caagtgtgaa ctgaagttt cagattcgga tgctgacg
gg 2640
gactgaggcc agcgtgtccc agcccatgcc cctctgtctt cgtggagagt gttgtgtt
ga 2700
gcccatttag tagccgagtc ttgtcactct gtgccagcct cagtcctgtg tccccctt
tt 2760
ctctggttt
2769

<210> 3
<211> 862
<212> PRT
<213> Human

<400> 3
Met Arg Met Cys Thr Pro Ile Arg Gly Leu Leu Met Ala Leu Ala Val
1 5 10 15
Met Phe Gly Thr Ala Met Ala Phe Ala Pro Ile Pro Arg Ile Thr Trp
20 25 30
Glu His Arg Glu Val His Leu Val Gln Phe His Glu Pro Asp Ile Tyr
35 40 45
Asn Tyr Ser Ala Leu Leu Ser Glu Asp Lys Asp Thr Leu Tyr Ile
50 55 60
Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
65 70 75 80
Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ala Lys
85 90 95
Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
100 105 110
Arg Val Leu Gln Pro Leu Ser Ala Thr Ser Leu Tyr Val Cys Gly Thr
115 120 125
Asn Ala Phe Gln Pro Ala Cys Asp His Leu Asn Leu Thr Ser Phe Lys
130 135 140
Phe Leu Gly Lys Asn Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro
145 150 155 160
Ala His Ser Tyr Thr Ser Val Met Val Asp Gly Glu Leu Tyr Ser Gly
165 170 175

Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
 180 185 190
 Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu
 195 200 205
 Pro Ser Phe Val Phe Ala Asp Val Ile Arg Lys Ser Pro Asp Ser Pro
 210 215 220
 Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe Thr Glu Val Ser Val
 225 230 235 240
 Glu Tyr Glu Phe Val Phe Arg Val Leu Ile Pro Arg Ile Ala Arg Val
 245 250 255
 Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr
 260 265 270
 Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Arg Pro Asp Ser Gly Leu
 275 280 285
 Val Phe Asn Val Leu Arg Asp Val Phe Val Leu Arg Ser Pro Gly Leu
 290 295 300
 Lys Val Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val
 305 310 315 320
 Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val
 325 330 335
 Phe Ser His Gly Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His
 340 345 350
 Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly
 355 360 365
 Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu
 370 375 380
 Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met
 385 390 395 400
 Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Arg Leu Ile Lys Lys
 405 410 415
 Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp
 420 425 430
 Gly Thr Val Tyr Asp Val Met Phe Val Ser Thr Asp Arg Gly Ala Leu
 435 440 445
 His Lys Ala Ile Ser Leu Glu His Ala Val His Ile Ile Glu Glu Thr
 450 455 460
 Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu Leu Leu Ser Ser
 465 470 475 480
 Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val
 485 490 495
 Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu Asp Cys
 500 505 510
 Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Pro Thr Ala Thr
 515 520 525
 Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln
 530 535 540
 Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser
 545 550 555 560
 Tyr Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys
 565 570 575
 Ser Gln Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly
 580 585 590

Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn
595 600 605
Leu Leu Ile Phe Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys
610 615 620
Leu Ser Glu Glu Arg Val Lys Asn Lys Thr Val Phe Gln Val Val Ala
625 630 635 640
Lys His Val Leu Glu Val Lys Val Val Pro Lys Pro Val Val Ala Pro
645 650 655
Thr Leu Ser Val Val Gln Thr Glu Gly Ser Arg Ile Ala Thr Lys Val
660 665 670
Leu Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Val Gln
675 680 685
Ala Thr Ser Ser Gly Ala Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr
690 695 700
Gly Thr Ser Cys Glu Pro Lys Ile Val Ile Asn Thr Val Pro Gln Leu
705 710 715 720
His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu
725 730 735
Met Ser Leu Phe Leu Phe Phe Val Leu Phe Leu Cys Leu Phe Phe
740 745 750
Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg
755 760 765
Ser Ala Leu Leu Ile Gly Lys Lys Pro Lys Ser Asp Phe Cys Asp
770 775 780
Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser
785 790 795 800
Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu
805 810 815
Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp
820 825 830
Ser Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val
835 840 845
Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
850 855 860

<210> 4
<211> 4157
<212> DNA
<213> Human

<400> 4
ctgagccgca tctgcaatag cacacttgcc cggccacctg ctgccgtgag cctttgct
gc 60
tgaagccctt ggggtcgccct ctacctgatg aggatgtgca cccccattag ggggctgc
tc 120
atggcccttg cagtgtatgtt tgggacagcg atggcatttg caccataacc ccggatca
cc 180
tgggagcaca gagaggtgca cctgggtgcag tttcatgagc cagacatcta caactact
ca 240
gccttgctgc tgagcgagga caaggacacc ttgtacatag gtgcccggga ggcggct
tc 300
gctgtgaacg cactcaacat ctccgagaag cagcatgagg tgtattggaa ggtctcag

aa 360
gacaaaaaag caaaatgtgc agaaaagggg aaatcaaaac agacagagtgcctcaact
ac 420
atccgggtgc tgccagccact cagcgccact tcccttacg tgtgtggac caacgcac
tc 480
cagccggcct gtgaccacccat gaacttaaca tcctttaagt ttctgggaa aaatgaag
at 540
ggcaaaggaa gatgtccctt tgacccagca cacagctaca catccgtcat gggtttagt
ga 600
gaactttatt cggggacgatc gtataatttt ttgggaagtgc aaccatcat ctcccgaa
at 660
tcttcccaca gtcctctgag gacagaatat gcaatccctt ggctgaacga gcctagtt
tc 720
gtgtttgctg acgtgatccg aaaaagccca gacagccccg acggcgagga tgacaggg
tc 780
tacttcttct tcacggaggt gtctgtggag tatgagtttgc ttgcagggt gctgatcc
ca 840
cgatagcaa gagtgtgcaa gggggaccag ggccgcctga ggacccatgcga gaagaaat
gg 900
accccttcc taaaagcccg actcatctgc tcccgccag acagccgtt ggtcttca
at 960
gtgctgcggg atgtttcgt gtcagggtcc cccggcctga aggtgcctgt gttctatgc
ca 1020
ctttcaccc cacagctgaa caacgtgggg ctgtcgccag tgcgcctcta caacctgt
cc 1080
acagccgagg aggtcttctc ccacgggaag tacatgcaga gcaccacagt ggagcagt
cc 1140
cacaccaagt gggtgcgcta taatggcccg gtacccaagc cgccgcctgg agcgtgca
tc 1200
gacagcgagg cacggccgc caactacacc agtccttgc atttgccaga caagacgc
tg 1260
cagttcgtta aagaccaccc tttgatggat gactcggtaa ccccaataga caacaggg
cc 1320
agtttaatca agaaagatgt gaactacacc cagatcggtgg tggaccggac ccaggccc
tg 1380
gatgggactg tctatgtatgt catgtttgtc agcacagacc gggagctct gcacaaag
cc 1440
atcagcctcg agcacgctgt tcacatcatc gaggagaccc agctttcca ggactttg
ag 1500
ccagtcaga ccctgctgct gtcttcaaag aaggcaaca gtttgccta tgctggct
ct 1560
aactcgcccg tggccaggc cccgctggcc ttctgtggaa agcacggcac ctgcgagg
ac 1620
tgtgtgtgg cgcgggaccc ctactgcgc tggagccgc ccacagcgac ctgcgtgg
ct 1680
ctgcaccaga ccgagagccc cagcagggtt tgattcagg agatgagcgg cgatgctt
ct 1740
gtgtgtcccg ataaaagtaa aggaagttac cggcagcatt tttcaagca cgggtggca
ca 1800
gcggaaactga aatgctccca aaaatccaac ctggcccggt tctttggaa gttccaga
at 1860
ggcgtgttgc agggcggagag ccccaagtac ggtcttatgg gcagaaaaaaa cttgctca

tc 1920
ttcaacttgt cagaaggaga cagtgggtg taccagtgcc tgtcagagga gagggta
ag 1980
aacaaaaacgg tcttccaagt ggtcgccaag cacgtcctgg aagtgaaggt ggttccaa
ag 2040
cccgtagtgtt ccccccaccc ttgttccatgtt cagacagaag gtagtaggat tgccacca
aa 2100
gtgttgtgg catccaccca agggtcttct cccccaaccc cagccgtgca ggccaccc
cc 2160
tccggggcca tcacccttcc tcccaagcct gcgcccaccc gcacatcctg cgaaccaa
ag 2220
atcgcatca acacggtccc ccagctccac tcggagaaaa ccatgtatct taagtcca
gc 2280
gacaaccggcc tcctcatgtc cctttccctc ttcttctttt ttcttccct ctgcctct
tt 2340
ttctacaact gctataaggg atacctgccc agacagtgc tgaaattccg ctcggccc
ta 2400
ctaattggga agaagaagcc caagtcagat ttctgtgacc gtgagcagag cctgaagg
ag 2460
acgttagtag agccagggag cttctccag cagaatgggg agcaccacca gccagccc
tg 2520
gacaccggct atgagaccga gcaagacacc atcaccagca aagtccccac ggataggg
ag 2580
gactcacaga ggatcgacga cctttctgccc agggacaagc ccttgacgt caagtgtg
ag 2640
ctgaagttcg ctgactcaga cgcagatgga gactgaggcc ggctgtgcat ccccgctg
gt 2700
gcctcggtcg cgacgtgtcc aggcgtggag agtttgtgt ttctcctgtt cagtatcc
ga 2760
gtctcgtgca gtgctgcgta ggttagcccg catcgtagcag acaacccctcag tcctcttg
tc 2820
tattttctct tgggttgagc ctgtgacttg gtttctctt gtccttttgg aaaaatga
ca 2880
agcattgcat cccagtcttg tgccctgaa tcagtcggag tacttgaaga aggcccac
gg 2940
gcggcacgga gttccctgagc cctttctgtt gtggggggaaa ggtggctgga cctctgtt
gg 3000
ctgagaagag catcccttca gcttcccctc cccgtacgag ccactaaaag attattta
at 3060
tccagattgg aaatgacatt ttagtttac agattggtaa cttatcgct gttgtcca
ga 3120
ttggcacgaa cctttcttc cacttaatta tttttttagg atttgcttt gattgtgt
tt 3180
atgtcatggg tcattttttt ttagttacag aagcagttgt gttaatattt agaagaag
at 3240
gtatatcttc cagattttgt tatatatttg gcataaaaata cggcttacgt tgcttaag
at 3300
tctcagggat aaacttcctt ttgctaaatg cattttttct gcttttagaa atgttagac
at 3360
aaacactccc cggagccac tcacctttt tctttttctt tttttttt taacttta
tt 3420
ccttgaggga agcattgttt ttggagagat tttcttctg tacttcgttt tacttttc

tt 3480
tttttttaac ttttactctc tcgaagaaga ggacccccc acatccacga ggtgggtt
tt 3540
gagcaaggga aggtagcctg gatgagctga gtggagccag gctggcccag agctgaga
tg 3600
ggagtgcggt acaatctgga gcccacagct gtcggtcaga acctcctgtg agacagat
gg 3660
aaccttcaca agggcgccctt tgggtctctg aacatctcct ttctcttctt gcttcaat
tg 3720
cttacccact gcctgcccag actttctatc cagcctcact gagctgccc a ctactgga
ag 3780
ggaactgggc ctcggtggcc gggccgcga gctgtgacca cagcaccctc aagcatac
gg 3840
cgctgttcct gccactgtcc tgaagatgtg aatgggtggt acgatttcaa cactggtt
aa 3900
tttcacactc catctccccg ctttgtaaat acccatcgaa aagagacttt tttccat
gg 3960
tgaagagcaa taaactctgg atgtttgtgc gcgtgtgtgg acagtcttat cttccagc
at 4020
gataggattt gaccattttg gtgtaaacat ttgtgtttta taagatttac cttgtttt
ta 4080
ttttctact ttgaattgta tacatttggaa aagtacccaa ataaatgaga agcttcta
tc 4140
ctaaaaaaaaaaaaaa
4157

<210> 5
<211> 361
<212> PRT
<213> Mouse

<400> 5
Met Ala Asp Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Val Pro
5 10 15
Leu Lys Asn Ser Ala Ser Asn His Leu Gly Gln Asp Cys Glu Ala Tyr
20 25 30
Glu Asp Gly Glu Leu Thr Tyr Glu Asn Val Gln Val Ser Pro Val Pro
35 40 45
Gly Gly Pro Pro Gly Leu Ala Ser Pro Ala Leu Ala Asp Lys Ala Gly
50 55 60
Val Gly Ser Glu Gln Pro Thr Ala Thr Trp Ser Ser Val Asn Ser Ser
65 70 75 80
Ala Leu Arg Gln Ile Pro Arg Cys Pro Thr Val Cys Leu Gln Tyr Phe
85 90 95
Leu Leu Gly Leu Leu Val Ser Cys Leu Met Leu Gly Val Ala Val Ile
100 105 110
Cys Leu Gly Val Arg Tyr Leu Gln Val Ser Arg Gln Phe Gln Glu Gly
115 120 125
Thr Arg Ile Trp Glu Ala Thr Asn Ser Ser Leu Gln Gln Gln Leu Arg
130 135 140
Glu Lys Ile Ser Gln Leu Gly Gln Lys Glu Val Glu Leu Gln Lys Ala
145 150 155 160

Arg Lys Glu Leu Ile Ser Ser Gln Asp Thr Leu Gln Glu Lys Gln Arg
165 170 175
Thr His Glu Asp Ala Glu Gln Gln Leu Gln Ala Cys Gln Ala Glu Arg
180 185 190
Ala Lys Thr Lys Glu Asn Leu Lys Thr Glu Glu Glu Arg Arg Arg Asp
195 200 205
Leu Asp Gln Arg Leu Thr Ser Thr Arg Glu Thr Leu Arg Arg Phe Phe
210 215 220
Ser Asp Ser Ser Asp Thr Cys Cys Pro Cys Gly Trp Ile Pro Tyr Gln
225 230 235 240
Glu Arg Cys Phe Tyr Ile Ser His Thr Leu Gly Ser Leu Glu Glu Ser
245 250 255
Gln Lys Tyr Cys Thr Ser Leu Ser Ser Lys Leu Ala Ala Phe Asp Glu
260 265 270
Pro Ser Lys Tyr Tyr Tyr Glu Tyr Leu Ser Asp Ala Pro Gln Val Ser
275 280 285
Leu Pro Ser Gly Leu Glu Glu Leu Leu Asp Arg Ser Lys Ser Tyr Trp
290 295 300
Ile Gln Met Ser Lys Lys Trp Arg Gln Asp Ser Asp Ser Gln Ser Arg
305 310 315 320
His Cys Val Arg Ile Lys Thr Tyr Tyr Gln Lys Trp Glu Arg Thr Ile
325 330 335
Ser Lys Cys Ala Glu Leu His Pro Cys Ile Cys Glu Ser Glu Ala Phe
340 345 350
Arg Phe Pro Asp Gly Ile Asn Leu Asn
355 360

<210> 6
<211> 1337
<212> DNA
<213> Mouse

<400> 6
tggaaagactg tgaagcagag gcgcggcagg ctatggctga cgctatcacg tatgcaga
cc 60
tgcgcgttgt gaaagtgcgg ctgaagaaca gcgcatactaa ccatcttagga caggactg
tg 120
aggcctatga agatggggaa ctcacctacg agaatgtgca agtgtctcca gtcccgagg
ag 180
ggccaccagg cttggcttcc cctgcactag cggacaaagc aggggtcggg tcagagca
ac 240
caactgcgac ctggagctct gtgaactcgt ctgctctcag gcagattccc cgctgtcc
ta 300
cagtctgctt gcaataacttc ttgcttggcc ttctcgtgtc ctgtctgatg ttaggggt
gg 360
ctgtcatctg cctggaggtt cgctatctgc aggtgtctcg gcagttccag gaggggac
ca 420
ggatttggga agccaccaat agcagcctgc agcagcagct cagggagaag ataagtca
gc 480
tggggcagaa ggaggtggag cttcagaagg ctcggaaaga gctgatctcg agccagga
ca 540
cattacagga gaagcagagg actcacgagg acgctgagca gcaactacaa gcctgcca

gg 600
ctgagagagc gaagaccaag gagaacctga aaactgagga ggagcggagg agggacct
gg 660
accagaggtt gacaagcacg cgggagacac tgagggcgctt cttctctgat tcatcaga
ca 720
cctgctgtcc atgcggatgg attccatatac aggaaaggtg ctttacatc tcacatac
cc 780
tcggaagtct ggaggagagc caaaaatact gcacatctct gtcctccaaa ctggcagc
at 840
tcgatgaacc ttctaagtat tactatgaag tttctctgcc cagcggctta gaggagtt
gc 900
tagatcggttc gaagtcatat tggatacaga tgagcaagaa gtggaggcag gactctga
ct 960
ctcaaagccg acattgtgtc aggataaaaa catattacca gaagtggaa agaacaat
tt 1020
ccaagtgtgc agagcttcac ccctgcattt gtgagtcgga ggcttcagg tttcctga
tg 1080
ggatcaatct gaactgaaac ggacacttga acaagacctt gtgacctaca tccttaac
ct 1140
acggcctgcc aatttttaag actgctattt ctccagcact ccctcactct cgggcatt
cc 1200
cagctaaggg atgacctgct gcttgcttga aagctgctcc agaaaactgga cttcttt
gg 1260
gaagagtaaa gaagcctcca gaaaagactt gacccctt aagaacttcc caaactag
ag 1320
atgggtcagg ggagggc
1337

<210> 7
<211> 359
<212> PRT
<213> Human

<400> 7
Met Ala Glu Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Ala Pro
5 10 15
Leu Lys Lys Ser Ile Ser Ser Arg Leu Gly Gln Asp Pro Gly Ala Asp
20 25 30
Asp Asp Gly Glu Ile Thr Tyr Glu Asn Val Gln Val Pro Ala Val Leu
35 40 45
Gly Val Pro Ser Ser Leu Ala Ser Ser Val Leu Gly Asp Lys Ala Ala
50 55 60
Val Lys Ser Glu Gln Pro Thr Ala Ser Trp Arg Ala Val Thr Ser Pro
65 70 75 80
Ala Val Gly Arg Ile Leu Pro Cys Arg Thr Thr Cys Leu Arg Tyr Leu
85 90 95
Leu Leu Gly Leu Leu Leu Thr Cys Leu Leu Leu Gly Val Thr Ala Ile
100 105 110
Cys Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr
115 120 125
Asn Arg Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg
130 135 140

Leu Lys Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser
145 150 155 160
Arg Arg Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg
165 170 175
Ala His Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg
180 185 190
Gln Lys Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala
195 200 205
Leu Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe
210 215 220
Thr Cys Gly Ser Ala Asp Thr Cys Cys Pro Ser Gly Trp Ile Met His
225 230 235 240
Gln Lys Ser Cys Phe Tyr Ile Ser Leu Thr Ser Lys Asn Trp Gln Glu
245 250 255
Ser Gln Lys Gln Cys Glu Thr Leu Ser Ser Lys Leu Ala Thr Phe Ser
260 265 270
Glu Ile Tyr Pro Gln Ser His Ser Tyr Tyr Phe Leu Asn Ser Leu Leu
275 280 285
Pro Asn Gly Gly Ser Gly Asn Ser Tyr Trp Thr Gly Leu Ser Ser Asn
290 295 300
Lys Asp Trp Lys Leu Thr Asp Asp Thr Gln Arg Thr Arg Thr Tyr Ala
305 310 315 320
Gln Ser Ser Lys Cys Asn Lys Val His Lys Thr Trp Ser Trp Trp Thr
325 330 335
Leu Glu Ser Glu Ser Cys Arg Ser Ser Leu Pro Tyr Ile Cys Glu Met
340 345 350
Thr Ala Phe Arg Phe Pro Asp
355

<210> 8
<211> 1531
<212> DNA
<213> Human

<400> 8
agtacacagag ggaacacaga gcctagttgt aaacggacag agacgagagg ggcaaggg
ag 60
gacagtggat gacagggaag acgagtgggg gcagagctgc tcaggaccat ggctgagg
cc 120
atcacctatg cagatctgag gtttgtaag gtcctctga agaagagcat ctccagcc
gg 180
ttaggacagg acccaggggc ttagtgcgtat gggaaatca cttacgagaa tttcaag
tg 240
cccgcatcctcc taggggtgcc ctcaagcttg gcttctctg tactagggga caaagcag
cg 300
gtcaagtccgg agcagccaaac tgcgtcctgg agagccgtga cgtcaccagc tgcgggc
gg 360
attctccctt gccgcacaac ctgcctgcga tacctcctgc tcggcctgct cttcacct
gc 420
ctgctgttag gagtgaccgc catctgcctg ggagtgcgtatctgcagggt gtctcagc
ag 480
ctccagcaga cgaacagggc tctgaaagtc actaacagca gcctgaggca gcagctcc

gc 540
ctcaagataa cgcaagctggg acagagtgc gaggatctgc aggggtccag gagagagc
tg 600
gcgcagagtc aggaagcact acaggtggaa cagagggctc atcaggcggc cgaaggc
ag 660
ctacaggcct gccaggcaga cagacagaag acgaaggaga cttgcaaag tgaggagc
aa 720
cagaggaggg cttggagca gaagctgagc aacatggaga acagactgaa gccttct
tc 780
acatgcggct cagcagacac ctgctgtccg tcggatgga taatgcata gaaaagct
gc 840
tttacatct cacttacttc aaaaaattgg caggagagcc aaaaacaatg tgaaactc
tg 900
tctccaagc tggccacatt cagtggaaatt tatccacaat cacactctta ctacttct
ta 960
aattcactgt tgccaaatgg tggtcaggg aattcatatt ggactggcct cagctcta
ac 1020
aaggattgga agttgactga tgatacacaa cgcacttagga cttatgctca aagctcaa
aa 1080
tgtaacaagg tacataaaac ttggcatgg tggacactgg agtcagagtc atgtagaa
gt 1140
tctctccct acatctgtga gatgacagct ttcaggttc cagattgga cagtcctt
tg 1200
cactgagttg acactcatgc caacaagaac ctgtgcccct cttcctaac ctgaggcc
tg 1260
gggtcctca gaccatctcc ttcattctgg gcagtgccag ccaccggctg acccacac
ct 1320
gacacttcca gccagtctgc tgcctgctcc ctcttcctga aactggactg ttcctggg
aa 1380
aagggtgaag ccacctctag aaggacttt ggcctcccc caagaacttc ccatggta
ga 1440
atgggtggg ggaggagggc gcacgggctg agcggatagg ggcggcccg agccagcc
ag 1500
gcagtttat tgaaatctt taaataatt g
1531

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 9
gctgtcgact gtgtgcccgt tgctgaaggc ct
32

<210> 10
<211> 53
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 10

gacggatcct acttactttg ctttgcttgc ttgagataca ccgtcttctc tga

53